METHOD OF PRODUCING VACCINES FROM PROTEIN SIGNAL OLIGOPEPTIDES

by: Matthias Rath, M.D.

This application is a continuation-in-part of U.S. patent application serial number 08/704,499 filed on August 28, 1996, which is a USC 371 of PCT/US95/00575 filed January 12, 1995, which is a continuation of patent application number 08/182,248, filed January 14, 1994, now abandoned.

Background

The discovery of the genetic code by Watson and Crick four decades ago defined the principles by which genes (the genetic code) encode for proteins by determining the sequence of amino acids. As is known, proteins are important carriers of metabolic information in living organisms. Exogenous protein organisms such as the HIV virus, and other endogenous proteins such as that which causes diabetes, are also the cause of many human diseases.

The genetic code determines the structure of proteins, thereby dictating the function of the protein. In the vast majority of proteins, biological activity and the specific function of the protein is primarily mediated via specific amino acid sequences located on the outside surface of the three dimensional protein.

The protein code determines the relation between structure and function within a protein sequence and, thereby effects a specific biological action. Therefore, the protein code is the biological language for protein-mediated information transfer during health and disease. The interaction of hormones and other ligands with their respective receptors, of enzymes with protein substrates, of adhesive proteins with integrins, and of antibodies with antigens, as well as other protein actions and interactions are determined by the same

structure/function principles and the same biological language. The protein code also provides a missing link in the regulation of protein synthesis. Proteins also have important feed-back functions directly or indirectly modulating the synthesis rate of that protein. The structure/function relation of proteins, which determines protein actions and interactions, are hereafter referred to as the protein code.

Conventional drug therapy is frequently compromised by an unknown therapeutic mechanism and by a wide range of side effects and considerable toxicity. Conventional gene therapy uses some of the protein interaction principles mentioned above to increase the therapeutic specificity of the pharmaceutical and the delivery of the drug to the target cells and organs, which results in a reduction in toxicity and safety compared to conventional drug therapy. However, gene therapy has its disadvantages as it requires that the specific sequence of the entire disease causing protein be determined. That is, in order to treat or fight a disease, scientists attempt to determine the genetic code by replicating the entire amino acid sequence of the disease causing protein. Gene therapy is compromised by its technological requirements and its high cost. The development of gene therapy drugs is a time consuming process through the research and development phase of the drug, the clinical studies phase, as well as in the drug manufacturing and therapy phase of the drugs so developed. For example, in gene therapy, identification of the target disease causing proteins spans anywhere from months to years. The production of a drug, in-vitro tests, in-vivo tests alone takes approximately another several years. First clinical studies span between 5 to 10 years. This causes drugs developed through gene therapy to be very expensive, and restricts its therapeutic application to only certain more profitable and exclusive areas of diseases in the foreseeable future.

Therefore, there is a need for a method of therapy that allows for the interception of pathological interactions with maximum effectiveness.

There is a further need for a method of therapy that enables maximum therapeutic specificity, based on the precise structure/function relation of specific oligopeptide signals.

Yet another need is for a method of therapy that is safe and eliminates or limits toxicity, and allows for controlling undesired biological side-effects by optimizing the length and composition of the therapeutic peptide.

There is also a need for a therapy method that reduced the time and expense of development of therapeutic peptides to a fraction of conventional gene therapeutic research and development. Most importantly, there is a need for a targeted and safe therapy method which will allow clinical application of drugs for a variety of disease causing proteins that have been ignored because of the cost of development.

Summary

Just as the human language allows for communication and interaction among humans, the protein code is the underlying communication means for the interaction of antigens with antibodies, enzymes with substrates, receptors with ligands, adhesion molecules with integrins and other forms of protein communication. Humans communicate through sentences. Sentences are in turn composed of words and words are in turn made of letters. Similarly, the three dimentional structure of proteins can be analogized to sentences through which protein communication takes place. The peptide sequence of the protein can be analogized to words in the sentence, and the individual amino acids of the protein can be analogized to letters in words. However, what today remains a mystery in the language of communication in proteins are the "verbs" of the protein code sentences.

The description discloses a method of producing therapeutic peptides as vaccines in the prevention of human disease which are caused by one or more proteins. This method of peptide therapy, in contrast to gene therapy, comprises identifying the protein responsible for causing the human disease; identifying one or more signal oligopeptide sequences within the structure of the disease causing protein, the one or more signal oligopeptides representing the amino acid sequence of maximum hydrophilicity; and synthesizing one or more vaccine oligopeptides, the vaccine oligopeptides having amino acid sequences corresponding to the amino acid sequences of the signal oligopeptides of maximum

hydrophilicity.

In an alternative embodiment the method further comprises a method of identifying one or more signal oligopeptide sequences within the structure of the disease causing protein, the one or more signal oligopeptides representing the amino acid sequence of maximum surface probability of the amino acids in the disease causing protein. The area of maximum surface probability defined as that portion of the amino acid sequence that has a higher probability of being on the surface of the protein.

In an alternative embodiment, the method further comprises a method of identifying one or more signal oligopeptide sequences within the structure of the disease causing protein, the one or more signal oligopeptides representing the amino acid sequence of maximum electrical charge of the amino acids in the disease causing protein.

The method further comprising an optimization step, wherein the one or more vaccine oligopeptides are manipulated through one or more amino acid residue substitutions, amino acid deletions, or amino acid insertions, or any combination thereof, to produce an optimized immunogenic response in vaccinated humans.

Preferably, the method of the invention comprises a method wherein immunogenic response of the vaccine oligopeptides in humans is enhanced by repetition of the vaccine oligopeptides to form a linear polypeptide.

Also, preferably, the method of the invention comprises a method wherein the immunogenic response of the vaccine oligopeptides in humans is enhanced by repetition of the vaccine oligopeptides to form a cyclic polypeptide.

In yet another preferred embodiment, the method of the invention comprises a method wherein the immunogenic response of the vaccine oligopeptides in humans is enhanced by coupling of one or more of the vaccine oligopeptides to an immunogenic

protein or non-protein haptens.

In yet another embodiment of the invention, the method of the invention comprises a method wherein the area of maximum hydrophilicity is identified by one or more hydrophilicity determining algorithms such as those identified in Table 1.

Advantages of Peptide Therapy over Gene Therapy and Drug Therapy

Peptide therapy will open a new field of therapeutic options in medicine. For the first time, it will be possible to develop specific therapeutic agents, which target only the affected organ or cell system, without any side effects. Of particular advantage is the fast identification of the therapeutic peptides, its short development phase and the resultant low cost. Furthermore, this new therapeutic technology will allow for the control of many diseases that are currently untreatable.

The benefits of peptide therapy become more obvious especially when compared to gene therapy. Gene therapy requires that first a gene specific for a given disease be identified. Once identified, then the process requires that it be artificially reproduced and then it be re-introduced into the patient's body. This procedure is both time consuming and its outcome is indeterminable. Thus, the therapeutic efficacy of gene therapy, can only be achieved after years of research and development and treatment, if at all.

In contrast, peptide therapy is based on the principle that at some point, the genetic code must be translated into proteins that then interact with cells, and that heath or disease is ultimately decided at the level of proteins. The identification and therapeutic use of the key oligopeptides within a selected protein is the most direct, specific, effective, as well as the safest and most affordable way for the prevention or treatment of the disease. Compared to gene therapy, the application of peptide therapy will shorten the time for development and treatment for many human diseases. Therefore, peptide therapy as described below has the following advantages.

Peptide therapy is a highly effective form of treatment. The discovery of the peptide code provides the rationale for deciphering the communication code of proteins in health and disease. This discovery is used therapeutically to intercept pathological interactions of human disease with maximum effectiveness.

Peptide therapy also enables maximum therapeutic specificity. Based on the precise understanding of the structure/function relation of specific protein signals, peptide therapy allows therapeutic targeting with unprecedented specificity.

Furthermore, peptide therapy is extremely safe. The use of synthetic analogs to physiologic compounds essentially eliminates the problem of toxicity. Possible undesired biological side-effects are controllable by optimizing the length and composition of the therapeutic peptide.

Time and expenses for the development of therapeutic peptides is a fraction of conventional therapeutic research and development. Identification of potential therapeutic peptides takes minutes; in vitro screening of potential peptides is a matter of weeks; animal studies should provide first in vivo results within a few months. Most importantly, the unprecedented specificity and safety background of peptide therapy will allow clinical studies without delay.

The advantages of peptide therapy become even more obvious when this novel therapeutic approach is compared to conventional therapies. Conventional drug therapy is frequently compromised by an unknown therapeutic mechanism and by a wide range of side effects and considerable toxicity. Gene therapy is compromised by limited availability, its technological requirements and its high costs, which restricts its therapeutic application to exclusive areas in the foreseeable future. Heterologous or synthetic antibody therapy, the therapeutic application of antibodies produced outside of the patient's body, can cause incalculable adverse reactions by the patient's immune system against these 'foreign' antibodies. In contrast, peptide therapy makes elegant use of the patient's own immune

system thereby excluding adverse immunological reactions.

Brief Description of Tables and Figures

Table 1; shows the various amino acids found in proteins and their hydrophilicity and surface probability values.

Fig.1A and 1B show several of the protein code interaction principles including legibility, accessibility, variability, and specificity. **Fig. 1C** shows the oppositely charged amino acids can attract each other thereby enhancing confirmational specificity. Figure **1D** shows vaccines stimulating the production of antibodies which block pathological communication pathways not only in the prevention and treatment of infectious diseases but also in the therapy of neoplastic diseases, metabolic disorders and other diseases.

Fig. 2 shows the method of this invention used in peptide therapy in diabetes. This figure shows the three hydrophilicity peaks in the glucagon precursor sequence (A,B,C).

Fig. 3 shows Peptide therapy in HIV infections. Synthetic analogs to signal oligopeptides of the HIV envelope protein GP 160 or the cell receptor CD4 are used as vaccines. The hydrophylicity blot revealing potential signal oligopeptide sequences of GP 160 is shown in the upper part of figure 3. [I don't have this]

Fig. 4 shows the method of this invention used in Direct Peptide Interception Therapy (Direct PIT).

Fig. 5 shows the method of this invention used in Indirect Peptide Interception Therapy (Indirect PIT) and optimization of the therapeutic peptide size or sequence by amino acid residue substitution, deletion and/or insertions.

Fig. 6 shows the method of this invention used in Peptide Regulation Therapy (PRT) including the methods for identification, design, development and therapeutic use of synthetic analogs to signal oligopeptides as negative feed-back regulators for the synthesis rate of selected proteins.

Fig. 7 shows the method of the present invention used in the development of In-Vitro Diagnostic Assays.

Fig. 8 shows the method of the present invention as described in Example No. 1.

Detailed Description

Infectious diseases, cancer, cardiovascular and other human diseases develop by means of one or more pathogenicity-mediating proteins, or disease causing proteins. Blocking the action of these proteins allows the specific therapeutic interception of a pathological communication, thereby blocking disease propagation.

In the human language eliminating or changing the verb of a sentence renders the whole sentence meaningless. Similarly, blocking the protein code verbs (signal oligopeptide sequences) can be therapeutically used to block the undesired action or interaction of an entire protein. If the verb in any sentence is altered, i.e. change eating to walking, the entire meaning of the sentence changes, or the sentence is rendered unintelligible. These verbs of the protein code, referred to as signal oligopeptides, determine the very specific function of a protein. Similarly, if a signal oligopeptide is altered (or blocked) in any given protein, either that protein's function changes, or the protein is rendered function-less. Interference with signal oligopeptides, these verbs of the protein code sentences, can lead to substantial modification or loss of the biological message of a protein. This modification or loss of the biological message of the protein can be used in peptide therapy to the advantage of a patient.

The specific action of these oligopeptides is determined by a characteristic combination of shape and electrical charge (both anionic and cationic) within the same signal sequence. Protein information transfer and protein interaction is dependent on the accessibility of the signal oli:gopeptide sequence. Therefore, in the majority of proteins, the sequence signals are localized on the surface of the protein. Signal oligopeptides are enriched with charged amino acids such as cationic amino acid residues arginine and lysine and/or the anionic amino acid residues glutamate and aspartate. Sometimes, these signal oligopeptides are in a versatile arrangement with neutral spacer amino acids. Therefore, signal oligopeptide sequences are generally represented by the regions of maximum hydrophilicity on the surface of the protein molecule.

A new type of signal is represented by oligopeptides which obtain their characteristic conformation or shape by a specific arrangement of oppositely charged amino acid residues within this oligopeptide sequence. These residues with opposite charge can attract each other thereby modulating a characteristic folding of this signal sequence. For example, in the signal sequence RGD the cationic residue arginine and the anionic residue aspartate attract each other leading to a characteristic folding of this tripeptide around the 'spacer' residue glycine.

The specific metabolic function of a protein is dependent on the specificity of its biological signal oligopeptide. The signal character of a specific signal oligopeptide is determined by a characteristic combination of electrical charge with structural conformation. Within a protein, RGD and analogous tripeptides can serve as strong primary anchors while the specific biological message is mediated by additional longer and more complex signal oligopeptides.

Synthetic analogs of signal oligopeptide sequences are used therapeutically in several ways. First, synthetic analogs of signal oligopeptide sequences can be used as competitive inhibitors of pathological communication. Second, synthetic analogs of signal oligopeptides can be used as vaccines. This second therapeutic approach makes use of the fact that signal oligopeptides on the surface of the protein are identical with the antigenicity determining lepitopes of this protein. Thus, antibodies are interceptors of metabolic communication. Binding the signal oligopeptide sequence of a protein to antibodies and other mediators of immune response reduces or blocks its metabolic interaction. If synthetic analogs to signal oligopeptides are used as vaccines it is necessary to render these peptides antigenic and to allow their discrimination as 'non-self . Synthetic analogs to signal oligopeptides can be rendered immunogenic by coupling them to haptens or by other conventional methods.

The method of this invention using synthetic analogs is based on the discovery of the primary structural principles determining immunogenicity. The discrimination between self

and non-self between species of animals and humans is primarily based on amino acid residue substitutions or other residue variations within the signal oligopeptide sequences of a protein. By making use of this discovery effective therapeutic signal oligopeptides can be rapidly produced in the following way: signal oligopeptides of a given protein in one species of animals are the antigenicity determinants of this protein in another species of animals. To block the action of a pathogenicity-mediating or disease causing protein in the treatment of a human disease the synthetic signal oligopeptide vaccines are designed by copying corresponding amino acid signal sequences from another species. A glucagon signal oligopeptide vaccine for the treatment of diabetic patients would be based on glucagon signal sequences from rabbits, sheep, mice or other species. A titration of the therapeutic efficiency is possible using the evolutionary chain method described below. The greater the genetic and evolutionary distance of the selected animal species to humans the greater its antigenicity and, consequently, the greater its therapeutic efficiency as a vaccine.

Furthermore, signal oligopeptides of a protein are identical with the potential antigenic determinants. Antibodies and other mediators of immune response are interceptors of specific biological communication. Signal oligopeptides as promoters of differentiated protein communication and immune response mediators as interceptors form sophisticated network of biological communication. Therefore, decoding the physiologic aspects of this communication network will lead to a precise understanding of millions of metabolic interactions including the principles for development and differentiation of the body, which will lead to the therapeutic control of many diseases and eventually their eradication as causes of human mortality.

Turning now to the figures the invention is described in detail. Figures 1A and 1B show principles upon which the protein code functions. Within the amino acid sequence of a disease cause protein one or more signal oligopeptides represent the "verbs" - of the protein code which determine the specific action and interaction of that protein. This is referred to as the legibility of the protein. The signal oligopeptides of a protein are enriched in electrically charged amino acids (either cationic or anionic) and represent a segment of

maximum hydrophylicity within the protein sequence. An infinite number of possible combinations between amino acids with different charges as well as neutral residues provide the variability for differentiated metabolic communication. The specificity of a signal sequence is the result of a characteristic combination of charge distribution and structural conformation within the signal oligopeptide sequence. Figure 1B shows the oppositely charged amino acids attracting each other thereby enhancing conformational. specificity. Signal oligopeptides mediate specific information transfer to their metabolic counterparts. Substitution, deletion or other amino acid residue variations within the signal sequence of a protein enable differentiation between 'self' and 'non-self'. Signal sequences are the antigenic epitopes of a protein and are responsible for
potential immune responses when exposed to other organisms. Direct and indirect Peptide Interception Therapy (PIT) can be used to intercept undesired or pathological communication and thereby block the disease. Figure 1C shows direct PIT synthetic analogs of signal oligopeptides used to competitively inhibit the interaction of proteins. Indirect PIT makes use of synthetic oligopeptides rendered immunogenic. Figure 1D shows vaccines stimulating the production of antibodies which block pathological communication pathways not only in the prevention and treatment of infectious diseases but also in the therapy of neoplastic diseases, metabolic disorders and other diseases.

Peptide Interception Therapy (PIT)

The metabolic interaction of proteins is primarily modulated by one or more oligopeptide signal sequences which determine the metabolic interaction of a protein. Peptide Interception Therapy (PIT) is defined as the specific therapeutic interception of pathological or undesired protein actions and interactions by the therapeutic use of synthetic analogs to the signal oligopeptide sequences of this protein. To intercept the undesirable action of the disease causing protein, only the signal oligopeptide (protein verb) of the disease causing protein is therapeutically blocked.

First, using conventional methods, a disease causing protein, such as Glucogon, which mediates diabetes, is identified. These signal oligopeptide sequences are located on

the surface of the disease causing protein and are represented by one or more sequences of maximum hydrophilicity region (e.g. hydrophilic maxima) or maximum electrical charge within the amino acid sequence of the protein. The signal oligopeptide sequences of this protein is identified from its primary structure by use of a protein data base in combination with a suitable algorithm, such as hydrophilicity or surface probability algorithms. Examples of hydrophilicity and surface probability algorithms are shown in Table 1. In this algorithm the highest hydrophilicity or probability values have to be assigned to the charged amino acids lysine, arginine, aspartate and glutamate followed by asparagine and glutamine.

Synthetic analogs to signal oligopeptide sequences can be therapeutically used to block the pathological effects of the disease causing protein. An unlimited number of signal oligopeptide analogs can be synthesized covering the entire sequence of a selected hydrophylicity peak or parts of it.

Table 1

Table 1: The Maxims of the Following Algorithms -or Modifications Thereof- Can Be Used to Determine Potential Signal Oligopeptides In the Primary Structure of a Protein From a Protein Sequence Database		
Amino Acid Residue	A. Hydrophylicity Algorithm *	B. Surface Probability Algorithm **
Arginine	3.0	9.5
Aspartate	3.0	8.1
Glutamate	3.0	8.4
Lysine	3.0	9.7
Aspartate or Asparagine	1.6	8.0
Glutamate or Glutamine	1.6	8.4
Serine	0.3	6.5
Asparagine	0.2	7.8
Glutamine	0.2	8.4
Glycine	0.0	4.8
Proline	0.0	7.5
Threonine	-0.4	7.0
Alanine	-0.5	4.9
Histidine	-0.5	6.6
Cysteine	-1.0	2.6
Methionine	-1.3	4.8
Valine	-1.5	3.6
Isoleucine	-1.8	3.4
Leucine	-1.8	4.0
Tyrosine	-2.3	7.6
Phenylalanine	-2.5	4.2
Tryptophan	-3.4	5.1
C. Algorithm Based on the Following Amino Acid Categories:		

1. Highest Values Assigned to Charged Amino Acids:	Aspartate, Glutamate, Lysine, Arginine, Histidine
2. Medium Values Assigned to Uncharged Polar Amino Acids:	Asparagine, Glutamine, Glycine, Cysteine, Serine, Threonine, Tyrosine
3. Lowest Values Assigned to Non Polar Amino Acids:	Alanine, Valine, Leucine, Isoleucine, Proline, Phenylalanine, Methionine, Tryptophan
*	According to HoppTP, Woods, KR. 1981. Proc. Natl. Acad. Sci. USA; 78: 3824-3828.
**	Boger. Proceedings of the 1988 Miami Bio/Technology Winter Symposium. Oxford and Washington. IRL Press.

Signal tetrapeptides, pentapeptides, hexapeptides and longer peptides represent primary candidates for specific peptide therapy. Shorter peptides, such as the tripeptide RGD, are less specific and ubiquitous side effects limit their broad therapeutic use.

Figure 2 shows the fundamentals of Peptide Interception Therapy (PIT). Proteins are essential carriers of specific metabolic information. Moreover, proteins are frequently mobile which makes them ideal and versatile communication molecules. This figure illustrates several key elements of direct PIT in peptide therapy. In conventional gene therapy, the entire three dimensional protein structure (protein sentence) is required to counter the effects of the disease causing protein. However, in direct peptide intercept therapy, only the signal oligopeptide sequence ("verb") has to be blocked. Figure 2 also shows methods for identification, design, development and therapeutic use of synthetic analogs to signal oligopeptides in Peptide Interception Therapy as direct competitive inhibitors of selected protein actions.

As further described in detail below, peptide Interception Therapy (PIT) is used in two principal ways: direct PIT, which uses synthetic analogs of signal oligopeptides as competitive inhibitors of pathological or undesired metabolic interaction; and indirect PIT, which uses synthetic analogs as vaccines to stimulate the production of specific antibodies. In indirect PIT, antibodies developed from vaccines, not the therapeutic peptide itself, function as interceptors of protein communication.

<u>**Use of Signal Oligopeptide Sequences in Direct Peptide Interception Therapy (DPIT)**</u>

As indicated above, Direct Peptide Interception Therapy (Direct PIT) uses synthetic analogs of signal oligopeptides as direct competitive inhibitors for undesired protein communication. Direct blocking of pathogenicity mediating protein communication leads to the control of the related disease or clinical condition. This therapeutic approach is preferentially used in acute conditions, e.g. antithrombotic or fibrinolytic therapy. Direct PIT

is preferentially used intravenously in higher therapeutic dosages of the synthetic peptide. Poly-oligopeptide analogs, time release delivery systems and other modifications of the peptide delivery mechanism are used to extend the range of various therapeutic applications.

Figure 2 demonstrates a method of peptide therapy in diabetes and the signal sequences of proglucagon and therapeutic alternatives for peptide therapy in diabetic patients. Conventional treatment in diabetes focuses on increased availability of insulin. Peptide therapy enables an alternative approach. Synthetic analogs to the signal sequences of glucagon can be therapeutically used to attenuate the effect of this insulin antagonist. Note the three hydrophilicity peaks in the glucagon precursor sequence (A, B, C). The mature glucagon hormone is activated by contact and charge redistribution within peaks A and C. PIT therapy could have two distinct targets. First, blocking charge redistribution of precursor molecule (PIT for Peak A or C) prevents activation of the precursor to mature hormone. PIT targeting peak B prevents the action of the glucagon hormone. Second, vaccination with synthetic glucagon signal oligopeptides rendered immunogenic by the described methods in this disclosure, or other suitable methods known in the art, is a baseline treatment for diabetic patients.

Figure 3 shows the steps taken in order to use the are of maximum hydrophilicity of the protein sequence (signal oligopeptide) to develop synthetic analogs to the signal oligopeptide for use as competitive inhibitors.

Use of Signal Oligopeptide Sequences in Indirect Peptide Interception Therapy (IPIT)

Today vaccines are essentially limited to prophylactics and therapy of infectious diseases. Heterologous or synthetic antibody therapy, the therapeutic application of antibodies produced outside of the patient's body, can cause incalculable adverse reactions by the patient's immune system against these 'foreign' antibodies.

Peptide therapy using indirect PIT enables the extension of the preventive and therapeutic use of vaccines to all areas of medicine. The great advantage of oligopeptide vaccines as compared to conventional vaccines, is that the entire protein is not used as a vaccine. Only synthetic analogs to one or more of the signal oligopeptides of the selected protein are used to produce the vaccine. Peptide therapy by targeting the signal oligopeptide sequence "verbs" of the disease causing protein, makes elegant use of the patient's own immune system thereby excluding adverse immunological reactions.

Indirect PIT is implemented in the following manner. Signal oligopeptides of a given protein in one species of animals are the antigenic epitopes of this protein for the immune system of another species. To block the action of a pathogenicity-mediating protein in the treatment of a human disease, the amino acid residue sequence of the oligopeptide vaccines should be homologous to the signal sequences of the same protein -but from another species of animals. Thus, a glucagon signal oligopeptide vaccine for the treatment of diabetic patients would be based on the glucagon signal sequences from rabbits, sheep, mice or other species. The aim of this residue manipulation is to create an antigenic epitope without compromising the ability of the antibodies produced to effectively block the metabolic interaction of the protein. This therapeutic approach mimics nature's way to discriminate between'self and'non-self and make therapeutic use of it.

Indirect PIT is based on the therapeutic use of antibodies produced by the patient's own immune system against the signal oligopeptide sequences of proteins mediating pathogenicity for undesired metabolic action. Indirect PIT is preferentially used for preventive therapy for the treatment of chronic conditions or as adjuncts to direct PIT or other forms of acute therapy.

Figure 4 shows peptide therapy in HIV infections. First, the HIV envelope protein GP 160 or the cell receptor CD4 is identified. The area of maximum electrical charge of the HIV envelope protein is then determined using the hydrophylicity blot which reveals potential signal sequences of GP 160 is used to identify the areas of maximum hydrophilicity

and maximum electrical charge. Synthetic analogs to signal oligopeptides of the HIV envelope protein GP 160 or the cell receptor CD4 are then used as vaccines. The specific antibodies produced effectively inhibit the infection of cells. Other targets of HIV peptide therapy are the regulator proteins Rev and Tat with the aim to block viral replication.

Figure 5 shows the principles of Indirect Peptide Interception Therapy (Indirect PIT) including the methods for identification, design, development and therapeutic use of synthetic analogs to signal oligopeptides in Peptide Interception Therapy as vaccines to stimulate a specific immune response with the aim to decrease or block selected protein actions.

<u>**Enhancement of Immunogenic Response in Indirect Peptide Therapy**</u>

The protein code is a key for individual development within a species as well as for the evolutionary diversification of species. The effectiveness of signal oligopeptides to mediate specific biological messages were the ultimate criterion for the evolutionary advantage of a protein and, thus, for the evolutionary survival of the gene encoding for it. Genetic mutations leading to the substitution of one or more amino acid residues within a signal oligopeptide sequence were an economic and therefore frequent mechanism to modulate and differentiate protein action and thereby promoting evolutionary diversification.

The signal oligopeptides of a given protein are identical with its potential antigenicity determining regions (antigenic epitopes). Furthermore, the primary mechanism determining antigenicity between different individuals and different species are amino acid residue substitutions, omissions and other residue variations within the signal oligopeptide sequence(s) of a protein.

As shown in Figure 5, the designer of therapeutic compounds for indirect PIT makes use of the evolutionary chain. The further apart two species of animals are in the evolutionary chain, the more: amino acid residue mutations occurred, including mutations in the signal oligopeptide sequences. Therefore, the further an animal species is from humans in

the evolutionary chain, the more antigenic is the therapeutic peptide derived from that animal. A titration of the therapeutic efficiency of indirect PIT is possible. Indirect PIT therapy with synthetic analogs to glucagon signal oligopeptides from a fish species is more effective than those from a mammalian species in blocking human glucagon action.

Therefore, an evolutionary comparison method is used, wherein one or more species of animals in an evolutionary chain are selected to produce different vaccine oligopeptides to the same disease causing protein. It is desired that each vaccine oligopeptide from the different species of animals produce a different immunogenic response in vaccinated humans. Thereafter, the vaccine oligopeptide that produced the desired immunogenic response in humans is selected for use in humans.

The protein code provides the basis for the immunological differentiation between humans and animal species. Substitutions, omissions, and other variations of one or more amino acid residues within the signal sequence of the protein enable an organism to differentiate between 'self' and 'non-self'. Thus, the protein code comprises the basic language of immunology.

Antigenicity required for effective indirect PIT therapy can also be stimulated in conventional ways, e.g. by omitting one or more amino acid residues at the N-terminal end of any given sequence (start of sequence), by omitting one or more amino acid residues at the C-terminal end of any given sequence (end of terminal), by omitting one or more amino acid residues at the N-terminal and the C-terminal end of any given sequence, by substituting one or more of the amino acid residues within any given sequence without consideration of charge and polarity of the substitution residue, by substituting one or more of the amino acid residues within any given sequences with amino acid residues with similar charge and/or polarity, by omitting one or more amino acid residues within any given sequence, by coupling the therapeutic peptides to defined haptens or other immunogenic compounds enhancing 'non-self recognition, or a combination of two or more of the mentioned methods.

Use of Signal Oligopeptide Sequences in Peptide Regulation Therapy (PRT)

A third therapeutic mechanism using synthetic analogs of signal oligopeptides is as feedback regulators for protein synthesis. Peptide Regulation Therapy (PRT) makes therapeutic use of synthetic analogs of signal oligopeptide sequences to decrease the synthesis rate of an undesired protein via feedback mechanisms. The synthesis rate of many proteins is determined by the amount of protein end-product available. The signal sequences of pathogenicity mediating proteins can be used to decrease the synthesis of this protein via direct or indirect feedback mechanisms.

Figure 6 shows the method of Peptide Regulation Therapy (PRT) including the methods for identification, design, development and therapeutic use of synthetic analogs to signal oligopeptides in Peptide Regulation Therapy as negative feedback regulators for the synthesis rate of selected proteins. Again, the area of maximum hydrophilicity of the protein sequence is determined using one of the following methods; hydrophilicity algorithm such as that described by Hobbs, Surface probability algorithm, any algorithm which assigns values to amino acid residues, higher charged amino acids receiving greater value over uncharged polar amino acid residues, over non-polar amino acids, or any combination of the above-mentioned methods.

Once the protein sequence's oligopeptide is identified, synthetic analogs are produced to match the sequence of the oligopeptide. If the synthetic analogs are not effective as feedback regulators, the analogs are optimized to produce the desired effect using peptide size alteration by amino acid residue substitution, deletion, insertion, or any combination thereof

Use of Signal Oligopeptide Sequences for Development of in vitro Diagnostics Kits

Polyclonal or monoclonal antibodies for a protein can be manufactured by first identifying the antigen. Synthetic analogs to one or more signal sequences of a proteins are used as antigens. These signal sequences are determined from a data base by making use of algorithms for hydrophylicity or surface probability. For clinical diagnostics the signal

sequence of the protein should preferentially be chosen from a database of human proteins.

To optimize specificity of the antigen the signal oligopeptide should be at least a tetrapeptide or preferentially longer oligopeptides. Polyclonal or monoclonal antibodies are then raised according to established methods using adjuvants or other haptens. The same synthetic signal oligopeptide analogs used as antigens can be used to test the specificity of the antibodies. Figure 7 shows the steps involved in the method of using Signal Oligopeptides sequences in in-vitro diagnostic assays.

<u>Use of Signal Oligopeptide Sequences in Theraneutic Applications of Peptide Therapy</u>

Infectious diseases. The most immediate application of peptide therapy is the prevention and treatment of infectious diseases. Every stage of any type of infectious disease is controlled by proteins which mediate adhesion, invasion and other mechanisms of pathogenicity. Effective therapeutic interception of biological signals within these pathogenicity-mediating proteins must lead to the control of the infection itself. As discussed above, for diseases mediated by xenologous proteins (infectious diseases) a signal sequence is chosen from xenologous protein (toxin) as basis for the vaccine in humans. The vaccines are then used for the prevention and treatment of the infectious disease.

Neoplastic Diseases. Another area with immediate applications for peptide therapy is the treatment of neoplastic diseases. Invasive growth and metastatic spread of any type of cancer is mediated by certain proteins and their signal sequences. Synthetic analogs to the signal sequences of these proteins should be developed as an effective therapy for different forms of cancer in their early stage as well as their invasive and metastatic stages.

Metabolic disorders. A novel therapeutic area for peptide therapy is the treatment of metabolic disorders. The potential of peptide therapy is exemplified here for the treatment of diabetes and hypertension, which are described in detail in the Examples

below.

1. Therefore, synthetic analogs to human signal oligopeptide sequences are used for;

a. as therapeutic agents for direct competitive inhibition of selected protein interaction,
b. as therapeutic agents in feedback regulation with aim to decrease the synthesis rate of the selected protein,
c. as therapeutic agents in combination with haptens or other conventional immunogens or adjuvents as vaccines stimulating a specific immune response which blocks or decreases the action of the selected protein, and
d. as antigens to produce antibodies against the selected human protein for invitro diagnostic purposes.

2. Synthetic analogs to protein signal sequences from other species are used;

a. as therapeutic agents (vaccines) in the prevention and treatment of human diseases, stimulating a specific immune response which blocks or decreases the action of the selected protein in the human body.
b. As therapeutic agents according to sections 1a and 1b above in the treatment of diseases in the respective animal species.
c. As antigens to produce antibodies against the selected protein for in vitro diagnostic purposes in the respective animal species.

Using the method of the invention as described above aids in the identification of potential therapeutic peptides in minutes; in vitro screening of potential peptides is a matter of weeks; and animal studies should provide first in vivo results within a few months.

<u>Example No. 1</u>

Conventional diabetic therapy aims at an increased availability of insulin. Peptide therapy allows a novel and alternative approach by inhibiting the action of glucagon, the

insulin antagonist. Amino acid sequence selection and therapeutic design of peptide vaccines for Indirect Peptide Interception Therapy, exemplified for the development of glucagon vaccines in clinical therapy of diabetes mellitus is described here.

The inhibition of glucagon is accomplished by using the therapeutic peptides analogous to the glucagon signal sequence for direct competitive inhibition or as a vaccine (Figure 2 and 8). First, the signal oligopeptide is identified from a human Glucagon Precursor sequence. Using the available data for Glucagon Precursor sequences in different species, a corresponding signal oligopeptide is identified to the human oligopeptide. Using the evolutionary tree, the relative distance of the available Glucagon Sequence to the human sequence is determined. The evolutionary distance is positively correlated with degree of amino acid variation and therefore, with the antigenicity of the selected protein.

The therapeutic peptide sequence is selected among the corresponding sequences according to the following criteria. If a moderate therapeutic immune response is desired, then the therapeutic signal sequence is preferably derived from species that are genetically close to humans (e.g. mammals). Amino acid residue variation within the therapeutic peptide (vaccine) is sufficient to cause immune response in humans. If a strong therapeutic response is desired, then the therapeutic peptides are designed from species that are genetically more distant to humans (e.g. Fish, Yeast). The more distant the species from humans, the more amino acid residue variation within the signal sequence, the greater the anitgenicity of therapeutic peptide, and the higher the therapeutic efficiency.

Example No. 2

The specific sequences described in this application as Sequence ID Nos. 1- 360 were selected using the method of the invention in order to provide specific treatments for common human diseases. The sequences so described are the signal oligopeptides characterized by a region of maximum hydrophilicity within the key protein known to mediate the indicated diseases.

For the prevention and treatment of atherosclerosis and cardioascular diseases, Therapeutic peptides from Apolipoprotein(a) (Sequence ID No.s 288 to 295). These peptides prevent the attachment of the most pathogenic lipoprotein fraction inside the artery walls, thereby preventing the formation of atherosclerotic plaques and cardiovascular diseases. Therapeutic peptides from apolioprotein(a) also competitivley detach lipoprotein(a) molecules from their binding sites inside the artery wall deposits, release them from the artery plaques and lead to the natural reversal of athereosclerosis and cardiovascular disease.

The therapeutic effect is achieved by direct application of the peptides as well as by using these peptides as vaccines and having the resulting antibodies block the binding sites. Therapeutic peptides from Farnesyl Synthetase (Sequence ID Nos. 1 to 41) and therapeutic peptides from Hydroxy-Methyl-Glutaryl Coenzyme A Reductase (Sequence ID No.s 42-95). These peptides attenuate two key enzymes of cholesterol synthesis, and are therapeutically used in patients with high cholesterol levels.

Example No. 3

The renin angiotensin system and particularly the angiotensin-converting enzyme (ACE) are a continuous focus of antihypertensive drug development. Renin, angiotensin I and II as well as ACE are also promising targets for peptide therapy. Therapeutic use of synthetic analogs to the signal sequences of any of these proteins will lead to decreased blood pressure. Since in most cases hypertension is a chronic condition the therapeutic use of renin, angiotensin or ACE signal peptide vaccines is a preferable method of treatment.

Example No. 4

For the acute treatment of myocardial infarction; therapeutic peptides from Plasminogen Activator Inhibitor (PAI-1) (Sequence ID Nos. 173 to 194) and Plasminogen Activator Inhibitor 2 (PAI-2) (Sequence ID Nos. 195-214) are used to block the physiological effect of plasminogen activator inhibitor, enhance plasminogen activation and thereby promote fibrinolysis. The preferred therapeutic application of the peptides in this

case is the intravenous injection of the peptides.

Example No. 5

The following proteins' signal sequences are derived from the method of this invention and are used for diagnostic as well as therapeutic purposes as described above.

Farnesyl Synthetase:	Sequence Id Nos. 1 - 41
Hydroxy-Methyl-Glutaryl Coenzyme A Reductase:	Sequence Id Nos. 42 - 163
Gonadoliberin Precursor	Sequence Id Nos. 164 - 172
Plasminogen Activator Inhibitor 1	Sequence Id Nos. 173 - 194
Plasminogen Activator Inhibitor 2	Sequence Id Nos. 195 - 238
Herpes Virus 1 (HSV 1) Glycoprotein B	Sequence Id Nos. 239 - 244
Herpes Virus 2 (HSV 23, 2H) Glycoprotein B	Sequence Id Nos. 245 - 251
Treponema Pallidum Membrane Protein (TMPA)	Sequence Id Nos. 252 - 262
Islet Amyloid Polypeptide	Sequence Id Nos. 263 - 268
Collagenase (Fibroblast MMP 1)	Sequence Id Nos. 269 - 280
Schistosoma, Elastase Precursor	Sequence Id Nos. 281 - 284
Schistosomin	Sequence Id Nos. 285 - 287
Apolipoprotein (a) Human	Sequence Id Nos. 288 - 289
Apolipoprotein (a) Rhesus	Sequence Id Nos. 290 - 295
Hepatitis Delta Antigen	Sequence Id Nos. 296 - 298
Rev Protein HIV, SIV, VILV, OMVVS	Sequence Id Nos. 299 - 348
Corticotropin Releasing Factor Binding Protein	Sequence Id Nos. 349 - 360